

SEQUENCE LISTING

<110> Meiji Seika Kaisha, Ltd.
<110> National Agriculture and Bio-oriented Research Organization

<120> Method for digesting proteins that highly resistant to denaturation and degradation

<130> MEJ-701

<150> JP 2002-309248
<151> 2002-10-24

<160> 4

<170> PatentIn version 3.1

<210> 1
<211> 825
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (1)... (825)
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cag gcc caa ggt tat aaa ggg gca aat gtc aaa gtc ggt atc att gat	96
Gln Ala Gln Gly Tyr Lys Gly Ala Asn Val Lys Val Gly Ile Ile Asp	
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acg gga atc gct tcg tct cat aca gac ttg aag gta gtc ggc gga gca	144
Thr Gly Ile Ala Ser Ser His Thr Asp Leu Lys Val Val Gly Gly Ala	
35 40 45	
agc ttt gta tct ggt gaa agt tat aat acg gac ggt aac gga cac ggc	192
Ser Phe Val Ser Gly Glu Ser Tyr Asn Thr Asp Gly Asn Gly His Gly	
50 55 60	

aca Thr 65	cat His	gtt Val	gcc Ala	gga Gly	aca Thr 70	gtg Val	gcg Ala	gcg Ala	ctt Leu	gac Asp 75	aat Asn	aca Thr	aca Thr	ggc Gly	gtt Val 80	240
tta Leu	ggc Gly	gtt Val	gca Ala	cgc Pro 85	aac Asn	gtc Val	tcc Ser	ctc Leu	tac Tyr 90	gcg Ala	att Ile	aag Lys	gtg Val	ttg Leu 95	aat Asn	288
tca Ser	agc Ser	gga Gly	agc Ser 100	gga Gly	aca Thr	tac Tyr	agc Ser	gca Ala 105	atc Ile	gtc Val	agc Ser	gga Gly	att Ile 110	gag Glu	tgg Trp	336
gcc Ala	aca Thr	caa Gln 115	aac Asn	ggc Gly	ctg Leu	gat Asp	gtc Val 120	atc Ile	aac Asn	atg Met	agc Ser	ctc Leu 125	ggc Gly	gga Gly	cca Pro	384
tcc Ser	ggc Gly 130	tca Ser	act Thr	gcg Ala	ctg Leu	aaa Lys 135	cag Gln	gct Ala	gtg Val	gat Asp	aaa Lys 140	gca Ala	tat Tyr	gcc Ala	agc Ser	432
gga Gly 145	att Ile	gtc Val	gta Val	gtg Val	gca Ala 150	gca Ala	gcg Ala	ggg Gly	aac Asn	agc Ser 155	gga Gly	tct Ser	tcc Ser	ggc Gly	agc Ser 160	480
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tca Ser	gag Glu 195	ctt Leu	gaa Glu	gtc Val	atg Met	gct Ala	cct Pro 200	ggc Gly	gtc Val	agc Ser	gta Val	tac Tyr 205	agc Ser	aca Thr	tat Tyr	624
cct Pro 210	tct Ser	aac Asn	acg Thr	tac Tyr	aca Thr	tca Ser 215	ttg Leu	aac Asn	gga Gly	act Thr	tca Ser 220	atg Met	gct Ala	tcg Ser	cct Pro	672
cat His 225	gta Val	gcg Ala	gga Gly	gca Ala	gca Ala 230	gcc Ala	ttg Leu	atc Ile	ttg Leu 235	tcg Ser	aaa Lys	tac Tyr	cct Pro	acg Thr	ctt Leu 240	720

tca gct tcc caa gtt cgc aac cgc ctc tca agc act gcg act aat ttg	768
Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Asn Leu	
245 250 255	

gga gat tcc ttc tac tac ggc aaa ggg ctg atc aat gta gaa gct gcc	816
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gct caa taa	825
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<210> 2
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 <213> *Bacillus licheniformis*

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Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
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Gln Ala Gln Gly Tyr Lys Gly Ala Asn Val Lys Val Gly Ile Ile Asp
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Thr Gly Ile Ala Ser Ser His Thr Asp Leu Lys Val Val Gly Gly Ala
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Ser Phe Val Ser Gly Glu Ser Tyr Asn Thr Asp Gly Asn Gly His Gly
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Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
65 70 75 80

Leu Gly Val Ala Pro Asn Val Ser Leu Tyr Ala Ile Lys Val Leu Asn
85 90 95

Ser Ser Gly Ser Gly Thr Tyr Ser Ala Ile Val Ser Gly Ile Glu Trp
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Ala Thr Gln Asn Gly Leu Asp Val Ile Asn Met Ser Leu Gly Gly Pro
 115 120 125

Ser Gly Ser Thr Ala Leu Lys Gln Ala Val Asp Lys Ala Tyr Ala Ser
 130 135 140

Gly Ile Val Val Val Ala Ala Ala Gly Asn Ser Gly Ser Ser Gly Ser
 145 150 155 160

Gln Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
 165 170 175

Gly Ala Val Asp Ser Asn Lys Asn Arg Ala Ser Phe Ser Ser Val Gly
 180 185 190

Ser Glu Leu Glu Val Met Ala Pro Gly Val Ser Val Tyr Ser Thr Tyr
 195 200 205

Pro Ser Asn Thr Tyr Thr Ser Leu Asn Gly Thr Ser Met Ala Ser Pro
 210 215 220

His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys Tyr Pro Thr Leu
 225 230 235 240

Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Asn Leu
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Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
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Ala Gln

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer PDE-2

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<210> 4
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<212> DNA
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<223> Description of Artificial Sequence: Primer PDE-5

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